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U. S. PATENT & TRADEMARK OFFICE

(B)

Tue Jul 17 13:24:30 2001 [BLASTP 2.1.3 [Apr-1-2001], NCBI]
/home/.../va/Molbio/carpenda/temp1/p1.DNA35639 (390 aa)

Sequences producing High-scoring Segment Pairs:

| | | Score | Match Pct | E-val |
|----|--|-------|-----------|-------|
| 1 | P_AAB53082 ✓ Human angiogenesis-associated protein PRO | 2012 | 390 100 | 0.0 |
| 2 | P_AAB80219 ✓ Human PRO246 protein - Homo sapiens. | 2012 | 390 100 | 0.0 |
| 3 | P_AAB31207 ✓ human polypeptide PRO246 - Homo sapiens. | 2012 | 390 100 | 0.0 |
| 4 | P_AAB68599 ✓ PRO246 - Homo sapiens. | 2012 | 390 100 | 0.0 |
| 5 | P_AAB88358 ✓ Human membrane or secretory protein clone | 2012 | 390 100 | 0.0 |
| 6 | P_AAY94999 ✓ Human secreted protein vc51_1, SEQ ID NO: | 2012 | 390 100 | 0.0 |
| 7 | P_AAY88574 ✓ Human PRO246 amino acid sequence - Homo s | 2012 | 390 100 | 0.0 |
| 8 | P_AAY05286 ✓ EGF-like homologue PRO246 - Homo sapiens. | 2012 | 390 100 | 0.0 |
| 9 | P_AAY13351 ✓ protein PRO246 - Homo sapiens. | 2012 | 390 100 | 0.0 |
| 10 | P_AAY27096 ✓ Human viral receptor protein (ACVRP) - Ho | 2012 | 390 100 | 0.0 |
| 11 | P_AAB90818 ✓ Human shear stress-response protein SEQ I | 2004 | 389 100 | 0.0 |
| 12 | P_AAY76303 ✓ Fragment of human secreted protein encode | 2003 | 388 100 | 0.0 |
| 13 | P_AAB65832 Human INTERCEPT 258 SEQ ID NO: 28 - Homo | 1734 | 341 94 | 0.0 |
| 14 | P_AAB65906 Human secreted protein related protein SE | 1732 | 340 94 | 0.0 |
| 15 | P_AAB65907 Human secreted protein related protein SE | 1730 | 340 94 | 0.0 |
| 16 | P_AAB65905 Human secreted protein related protein SE | 1730 | 340 94 | 0.0 |
| 17 | P_AAB65904 Human secreted protein related protein SE | 1730 | 340 94 | 0.0 |

>1 P_AAB53082 Human angiogenesis-associated protein PRO246, SEQ ID NO:96 - Homo sapiens. (390 aa) [1 seg]

Score = 2012 (779 bits), Expect = 0.0

Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

| | |
|------------|---|
| DNA35639 | 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV |
| ***** | |
| P_AAB53082 | 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV |
| ***** | |
| DNA35639 | 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD |
| ***** | |
| P_AAB53082 | 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD |
| ***** | |
| DNA35639 | 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK |
| ***** | |
| P_AAB53082 | 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK |
| ***** | |
| DNA35639 | 181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE |
| ***** | |
| P_AAB53082 | 181 PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE |
| ***** | |
| DNA35639 | 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS |
| ***** | |
| P_AAB53082 | 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS |
| ***** | |
| DNA35639 | 301 SDTISKNGTLSSVTSARALRPPHPPRGALTPPSLSSQALPSPLPTTDGAHPQPISP |
| ***** | |
| P_AAB53082 | 301 SDTISKNGTLSSVTSARALRPPHPPRGALTPPSLSSQALPSPLPTTDGAHPQPISP |
| ***** | |
| DNA35639 | 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV |
| ***** | |
| P_AAB53082 | 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV |

>2 P_AAB80219 Human PRO246 protein - Homo sapiens. (390 aa) [1 seg]

BLAST RESULTS B-1

Score = 2012 (779 bits), Expect = 0.0
 Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

| | | |
|------------|-----|--|
| DNA35639 | 1 | MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV ***** |
| P_AAB80219 | 1 | MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV ***** |
| DNA35639 | 61 | SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKD ***** |
| P_AAB80219 | 61 | SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKD ***** |
| DNA35639 | 121 | SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK ***** |
| P_AAB80219 | 121 | SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK ***** |
| DNA35639 | 181 | PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE ***** |
| P_AAB80219 | 181 | PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE ***** |
| DNA35639 | 241 | VSTGPGAAVVAGAVVGTLVGLLAGLVLLYHRRGKALEEPANDIKAIAAPRTLPWPKS ***** |
| P_AAB80219 | 241 | VSTGPGAAVVAGAVVGTLVGLLAGLVLLYHRRGKALEEPANDIKAIAAPRTLPWPKS ***** |
| DNA35639 | 301 | SDTISKNGTLSSVTSARALRPPHGPPRGALTPTPSLSSQALPSPLPTTDGAHPQPISP ***** |
| P_AAB80219 | 301 | SDTISKNGTLSSVTSARALRPPHGPPRGALTPTPSLSSQALPSPLPTTDGAHPQPISP ***** |
| DNA35639 | 361 | IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV ***** |
| P_AAB80219 | 361 | IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV ***** |

>3 P_AAB31207 human polypeptide PRO246'- Homo sapiens. (390 aa) [1 seg]
 Score = 2012 (779 bits), Expect = 0.0
 Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

| | | |
|------------|-----|--|
| DNA35639 | 1 | MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV ***** |
| P_AAB31207 | 1 | MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV ***** |
| DNA35639 | 61 | SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKD ***** |
| P_AAB31207 | 61 | SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKD ***** |
| DNA35639 | 121 | SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK ***** |
| P_AAB31207 | 121 | SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK ***** |
| DNA35639 | 181 | PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE ***** |
| P_AAB31207 | 181 | PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE ***** |
| DNA35639 | 241 | VSTGPGAAVVAGAVVGTLVGLLAGLVLLYHRRGKALEEPANDIKAIAAPRTLPWPKS ***** |
| P_AAB31207 | 241 | VSTGPGAAVVAGAVVGTLVGLLAGLVLLYHRRGKALEEPANDIKAIAAPRTLPWPKS ***** |
| DNA35639 | 301 | SDTISKNGTLSSVTSARALRPPHGPPRGALTPTPSLSSQALPSPLPTTDGAHPQPISP ***** |

P_AAB31207 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

P_AAB31207 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>4 P_AAB68599 PRO246 - Homo sapiens. (390 aa) [1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAB68599 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKD

P_AAB68599 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKD

DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

P_AAB68599 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

P_AAB68599 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTL PWPKS

P_AAB68599 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTL PWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPLPTTDGAHPQPISP

P_AAB68599 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

P_AAB68599 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>5 P_AAB88358 Human membrane or secretory protein clone PSEC0086 - Homo (390 aa) [1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAB88358 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKD

P_AAB88358 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKD

DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

P_AAB88358 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

P_AAB88358 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTL PWPKS

P_AAB88358 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTL PWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPTPSLSSQALPSPRLPTTDGAHPQPISP

P_AAB88358 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPTPSLSSQALPSPRLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

P_AAB88358 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>6 P_AAY94999 Human secreted protein vc51_1, SEQ ID NO:38 - Homo sapiens. (390 aa) [1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAY94999 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

P_AAY94999 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSK

P_AAY94999 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSK

DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

P_AAY94999 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTL PWPKS

P_AAY94999 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTL PWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPTPSLSSQALPSPRLPTTDGAHPQPISP

P_AAY94999 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPTPSLSSQALPSPRLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

P_AAY94999 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>7 P_AAY88574 Human PRO246 amino acid sequence - Homo sapiens. (390 aa) [1 seg]
Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAY88574 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

P_AAY88574 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD
 DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 P_AAY88574 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK
 DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

 P_AAY88574 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
 DNA35639 241 VSTGPGAAVVAGAVVGTLVGLLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS

 P_AAY88574 241 VSTGPGAAVVAGAVVGTLVGLLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS
 DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP

 P_AAY88574 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP
 DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

 P_AAY88574 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>8 P_AAY05286 EGF-like homologue PRO246 - Homo sapiens. (390 aa) [1 seg]
 Score = 2012 (779 bits), Expect = 0.0
 Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSLAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 P_AAY05286 1 MISLPGPLVTNLLRFLFLGLSLAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV
 DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD

 P_AAY05286 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD
 DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 P_AAY05286 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK
 DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

 P_AAY05286 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE
 DNA35639 241 VSTGPGAAVVAGAVVGTLVGLLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS

 P_AAY05286 241 VSTGPGAAVVAGAVVGTLVGLLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPWPKS
 DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP

 P_AAY05286 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP
 DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

 P_AAY05286 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>9 P_AAY13351 protein PRO246 - Homo sapiens. (390 aa) [1 seg]
 Score = 2012 (779 bits), Expect = 0.0
 Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

BLAST RESULTS B-19

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAY13351 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

P_AAY13351 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

P_AAY13351 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

P_AAY13351 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAIAAPRTLPWPKS

P_AAY13351 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAIAAPRTLPWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPTPSLSSQALPSPLPTTDGAHPQPISP

P_AAY13351 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPTPSLSSQALPSPLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

P_AAY13351 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>10 P_AAY27096 Human viral receptor protein (ACVRP) - Homo sapiens. (390 aa) [1 seg]

Score = 2012 (779 bits), Expect = 0.0
Identities = 390/390 (100%), Positives = 390/390 (100%), at 1,1-390,390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAY27096 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

P_AAY27096 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

P_AAY27096 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

P_AAY27096 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAIAAPRTLPWPKS

P_AAY27096 241 VSTGPGAAVVAGAVVGTLVGLGLAGLVLLYHRRGKALEEPANDIKAIAAPRTLPWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPTPSLSSQALPSPLPTTDGAHPQPISP

P_AAY27096 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPTPSLSSQALPSPLPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

 P_AAY27096 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>11 P_AAB90818 Human shear stress-response protein SEQ ID NO: 144 - Homo (390 aa) [1 seg]

Score = 2004 (776 bits), Expect = 0.0
 Identities = 389/390 (99%), Positives = 389/390 (99%), at 1,1-390, 390

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 P_AAB90818 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD

 P_AAB90818 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD

 DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 P_AAB90818 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

 P_AAB90818 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

 DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAIA PRTL PWPKS

 P_AAB90818 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAIA PRTL PWPKS

 DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP

 P_AAB90818 301 SDTISKNGTLSSVTSARALWPPHGPPRGALTPPSLSSQALPSPRLPTTDGAHPQPISP

 DNA35639 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

 P_AAB90818 361 IPGGVSSSGLSRMGAVPVMVPAQSQAGSLV

>12 P_AAY76303 Fragment of human secreted protein encoded by gene 29 - Homo (389 aa) [1 seg]

Score = 2003 (776 bits), Expect = 0.0
 Identities = 388/389 (99%), Positives = 389/389 (99%), at 1,1-389, 389

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 P_AAY76303 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD

 P_AAY76303 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLEGLQEKD

 DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 P_AAY76303 121 SGPYSCSVNVQNKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

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P_AAY76303 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIA PRTLPWPKS

P_AAY76303 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIA PRTLPWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPR LPTTDGAHPQPISP

P_AAY76303 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPR LPTTDGAHPQPISP

DNA35639 361 IPGGVSSSGLSRMGA VPVMVPAQSQAGSL

P_AAY76303 361 IPGGVSSSGLSRMGA VPVMVPAQSQAGSL

>13 P_AAB65832 Human INTERCEPT 258 SEQ ID NO: 28 - Homo sapiens. (370 aa) [1 seg]
Score = 1734 (672 bits), Expect = 0.0
Identities = 341/362 (94%), Positives = 344/362 (94%), Gaps = 7/362 (1%), at 1,1-355,362

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAB65832 1 MISLPGPLVTNLXRFLLGLSALAPPSRAQLQLHLPANRLQAVEEGESGASAWYTLHREV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKD

P_AAB65832 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRVEGLQEKD

DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

P_AAB65832 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

P_AAB65832 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIA PRTLPWPKS

P_AAB65832 241 VSTGPGAAVVAEAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIA PRTLPWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPR-----LPTTDGA

P_AAB65832 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRHAHDRWGPPSTNIP

DNA35639 354 HP
**

P_AAB65832 361 HP

>14 P_AAB65906 Human secreted protein related protein SEQ ID NO: 138 - Homo (370 aa) [1 seg]
Score = 1732 (671 bits), Expect = 0.0
Identities = 340/362 (93%), Positives = 344/362 (94%), Gaps = 7/362 (1%), at 1,1-355,362

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

P_AAB65906 1 MISLPGPLVTNLXRFLLGLSALAPPSRAQLQLHLPANRLQAVEEGESGASAWYTLHREV

DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

 P_AAB65906 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRVEGLQEKD

 DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 P_AAB65906 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRIQGVPHVGANVTLSCQSPRSK

 DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

 P_AAB65906 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

 DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAIA PRTL PWPKS

 P_AAB65906 241 VSTGPGAAVVAEAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAIA PRTL PWPKS

 DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPSLSSQALPSPR-----LPTTDGA
 ***** *.
 P_AAB65906 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPSLSSQALPSPRHAHDRWGPPSTNIP

 DNA35639 354 HP
 **
 P_AAB65906 361 HP

>15 P_AAB65907 Human secreted protein related protein SEQ ID NO: 140 - Homo (370
 aa) [1 seg]
 Score = 1730 (671 bits), Expect = 0.0
 Identities = 340/362 (93%), Positives = 343/362 (93%), Gaps = 7/362 (1%), at
 1,1-355,362

DNA35639 1 MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV

 P_AAB65907 1 MISLPGPLVTNLXRFFLGLSALAPPSRAQLQLHLPANRLQAVEEGESGASAWYTLHREV

 DNA35639 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKD

 P_AAB65907 61 SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRVEGLQEKD

 DNA35639 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 P_AAB65907 121 SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSK

 DNA35639 181 PAVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE
 * *****
 P_AAB65907 181 PVVQYQWDRQLPSFQTFFAPALD VIRGSLSLTNLSSMAGVYVCKAHNEVGTAQCNVTLE

 DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAIA PRTL PWPKS

 P_AAB65907 241 VSTGPGAAVVAEAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKAIA PRTL PWPKS

 DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPSLSSQALPSPR-----LPTTDGA
 ***** *.
 P_AAB65907 301 SDTISKNGTLSSVTSARALRPPHGPPRGALTPSLSSQALPSPRHAHDRWGPPSTNIP

 DNA35639 354 HP
 **

P AAB65907 361 HP

>16 P_AAB65905 Human secreted protein related protein SEQ ID NO: 136 - Homo (370
aa) [1 seg]
Score = 1730 (671 bits), Expect = 0.0
Identities = 340/362 (93%), Positives = 343/362 (93%), Gaps = 7/362 (1%), at
1,1-355,362

| | | |
|------------|-----|---|
| DNA35639 | 1 | MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV |
| P_AAB65905 | 1 | MISLPGPLVTNLXRFLFLGLSALAPPSRAQLQLHLPANRLQAVEEGESGASAWSYTLHREV |
| DNA35639 | 61 | SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYMPSPRNLSLRLEGLQEKD |
| P_AAB65905 | 61 | SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLAYSPSPRNLSLRVEGLQEKD |
| DNA35639 | 121 | SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSK |
| P_AAB65905 | 121 | SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSK |
| DNA35639 | 181 | PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE |
| P_AAB65905 | 181 | PAVQYQWDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE |
| DNA35639 | 241 | VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS |
| P_AAB65905 | 241 | VSTGPGAAVVAEAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS |
| DNA35639 | 301 | SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPR-----LPTTDGA |
| P_AAB65905 | 301 | SDTISKNGTLSSVTSARALRPPHGPPRGALTPPSLSSQALPSPRAHDRWGPSTNIP |
| DNA35639 | 354 | HP |
| P_AAB65905 | 361 | HP |

>17 P_AAB65904 Human secreted protein related protein SEQ ID NO: 134 - Homo (370
aa) [1 seg]
Score = 1730 (671 bits), Expect = 0.0
Identities = 340/362 (93%), Positives = 343/362 (93%), Gaps = 7/362 (1%), at
1,1-355,362

| | | |
|------------|-----|---|
| DNA35639 | 1 | MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEV ***** |
| P_AAB65904 | 1 | MISLPGPLVTNLXRFIFLGLSALAPPSRAQLQLHLPANRLQAVEEGESGASA |
| DNA35639 | 61 | SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEG ***** |
| P_AAB65904 | 61 | SSSQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRVEGL ***** |
| DNA35639 | 121 | SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQS ***** |
| P_AAB65904 | 121 | SGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQS ***** |
| DNA35639 | 181 | PAVQYQWDRQLPSFQTFFAPALDVI |
| P_AAB65904 | 181 | PAVQYQWDRQLPSFQTFFAPALDVI |

BLAST RESULTS Br-10

DNA35639 241 VSTGPGAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS

P_AAB65904 241 VSTGPGAAVVAEAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKS

DNA35639 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPR-----LPTTDGA
***** *.
P_AAB65904 301 SDTISKNGTLSSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRHAHDRWGPPSTNIP

DNA35639 354 HP
**
P_AAB65904 361 HP